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Sequence Listing was accepted.

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217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2009; month=3; day=13; hr=13; min=51; sec=47; ms=397; ]

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Application No: 10524234

Version No: 1.0

Input Set:

Output Set:

Started: 2009-02-20 19:08:00.629

Finished: 2009-02-20 19:08:02.730

Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 101 ms

Total Warnings: 19

Total Errors: 0

No. of SeqIDs Defined: 33

Actual SeqID Count: 33

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# SEQUENCE LISTING

<110> Blattmann, Beat O.  
 Darzins, Aldis  
 Davis, John M.  
 Encell, Lance P.  
 Morrison, Thomas B.  
 Mrachko, Gregory T.  
 Schellenberger, Volker

<120> Mutant E. Coli AppA Phytase Enzymes and  
 Natural Variants Thereof, Nucleic Acids Encoding Such  
 Phytase Enzymes, Vectors and Host Cells Incorporating Same  
 and Methods of Making and Using Same

<130> GC718-2-US

<140> 10524234  
 <141> 2009-02-20

<150> PCT/US03/25058  
 <151> 2003-08-11

<150> US 60/403,330  
 <151> 2002-08-12

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 Val Arg  
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 <212> PRT  
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Asp	Ala	Trp	Pro	Thr	Trp	Pro	Val	Lys	Leu	Gly	Trp	Leu	Thr	Pro	Arg
65					70					75					80
Gly	Gly	Glu	Leu	Ile	Ala	Tyr	Leu	Gly	His	Tyr	Gln	Arg	Gln	Arg	Leu
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Gln	Ala	Asp	Thr	Ser	Ser	Pro	Asp	Pro	Leu	Phe	Asn	Pro	Leu	Lys	Thr
145					150					155					160
Gly	Val	Cys	Gln	Leu	Asp	Asn	Ala	Asn	Val	Thr	Asp	Ala	Ile	Leu	Ser
				165				170						175	
Arg	Ala	Gly	Gly	Ser	Ile	Ala	Asp	Phe	Thr	Gly	His	Arg	Gln	Thr	Ala
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Val	Ser	Leu	Ala	Ser	Met	Leu	Thr	Glu	Ile	Phe	Leu	Leu	Gln	Gln	Ala
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Gln	Gly	Met	Pro	Glu	Pro	Gly	Trp	Gly	Arg	Ile	Thr	Asp	Ser	His	Gln
			260					265					270		
Trp	Asn	Thr	Leu	Leu	Ser	Leu	His	Asn	Ala	Gln	Phe	Tyr	Leu	Leu	Gln
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	290					295					300				
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Val	Thr	Leu	Pro	Thr	Ser	Val	Leu	Phe	Ile	Ala	Gly	His	Asp	Thr	Asn
				325					330					335	
Leu	Ala	Asn	Leu	Gly	Gly	Ala	Leu	Glu	Leu	Asn	Trp	Thr	Leu	Pro	Gly
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<213> Artificial Sequence

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<223> synthetic mutant AppA PHY679 phytase

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Glu	Pro	Glu	Leu	Lys	Leu	Glu	Ser	Val	Val	Ile	Val	Ser	Arg	His	Gly
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Val	Arg	Ala	Pro	Thr	Lys	Ala	Thr	Ala	Leu	Met	Gln	Asp	Val	Thr	Pro
					55						60				
Asp	Ala	Trp	Pro	Thr	Trp	Pro	Val	Lys	Leu	Gly	Trp	Leu	Thr	Pro	Arg
65					70					75					80
Gly	Gly	Glu	Leu	Ile	Ala	Tyr	Leu	Gly	His	Tyr	Gln	Arg	Gln	Arg	Leu
				85					90					95	
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			100					105					110		
Val	Ala	Ile	Ile	Ala	Asp	Val	Asp	Glu	Arg	Thr	Arg	Lys	Thr	Gly	Glu
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Ala	Phe	Ala	Ala	Gly	Leu	Ala	Pro	Asp	Cys	Ala	Ile	Thr	Val	Arg	Thr
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Gln	Ala	Asp	Thr	Ser	Ser	Pro	Asp	Pro	Leu	Phe	Lys	Pro	Leu	Lys	Thr
145					150					155				160	
Gly	Val	Cys	Gln	Leu	Asp	Asn	Ala	Asn	Val	Thr	Asp	Ala	Ile	Leu	Ser
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Arg	Ala	Gly	Gly	Ser	Ile	Ala	Asp	Phe	Thr	Gly	His	Arg	Gln	Thr	Ala
			180					185					190		
Phe	Arg	Glu	Leu	Glu	Arg	Val	Leu	Asn	Phe	Pro	Gln	Ser	Asn	Leu	Cys
		195					200					205			
Leu	Lys	Arg	Glu	Lys	Gln	Asp	Glu	Ser	Cys	Ser	Leu	Thr	Gln	Ala	Leu
		210				215					220				
Pro	Ser	Glu	Leu	Lys	Val	Ser	Ala	Asp	Asn	Val	Ser	Leu	Thr	Gly	Ala
225					230					235				240	
Val	Ser	Leu	Ala	Ser	Met	Leu	Thr	Glu	Ile	Phe	Leu	Leu	Gln	Gln	Ala
				245					250					255	
Gln	Pro	Met	Pro	Glu	Pro	Gly	Trp	Gly	Arg	Ile	Thr	Asp	Ser	His	Gln
			260					265				270			
Trp	Asn	Thr	Leu	Leu	Ser	Leu	His	Asn	Ala	Gln	Phe	Tyr	Leu	Leu	Gln
		275					280					285			
Arg	Thr	Pro	Glu	Val	Ala	Arg	Ser	Arg	Ala	Thr	Pro	Leu	Leu	Asp	Leu
		290				295					300				
Ile	Lys	Thr	Ala	Leu	Thr	Pro	His	Pro	Pro	Gln	Lys	Gln	Ala	Tyr	Gly
305					310					315				320	
Val	Thr	Leu	Pro	Thr	Ser	Val	Leu	Phe	Ile	Ala	Gly	His	Asp	Thr	Asn
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Leu	Ala	Asn	Leu	Gly	Gly	Ala	Leu	Glu	Leu	Asn	Trp	Thr	Leu	Pro	Gly
			340					345					350		
Gln	Pro	Asp	Asn	Thr	Pro	Pro	Gly	Gly	Glu	Leu	Val	Phe	Glu	Arg	Trp
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Arg	Arg	Leu	Ser	Asp	Asn	Ser	Gln	Trp	Ile	Gln	Val	Ser	Leu	Val	Phe
		370					375					380			

Gln	Thr	Leu	Gln	Gln	Met	Arg	Asp	Lys	Thr	Pro	Leu	Ser	Leu	Asn	Thr
385					390					395					400
Pro	Pro	Gly	Glu	Val	Lys	Leu	Thr	Leu	Ala	Gly	Cys	Glu	Glu	Arg	Asn
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<212> PRT

<213> Artificial Sequence

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<223> synthetic mutant AppA PHY735 phytase

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			20					25					30		
Glu	Pro	Glu	Leu	Lys	Leu	Glu	Ser	Val	Val	Ile	Val	Ser	Arg	His	Gly
	35					40					45				
Val	Arg	Ala	Pro	Thr	Lys	Ala	Thr	Gln	Leu	Met	Gln	Asp	Val	Thr	Pro
	50				55					60					
Asp	Ala	Trp	Pro	Thr	Trp	Pro	Val	Lys	Leu	Gly	Trp	Leu	Thr	Pro	Arg
65					70				75					80	
Gly	Gly	Glu	Leu	Ile	Ala	Tyr	Leu	Gly	His	Tyr	Gln	Arg	Gln	Arg	Leu
				85					90					95	
Val	Ala	Asp	Gly	Leu	Leu	Ala	Lys	Lys	Gly	Cys	Pro	Gln	Ser	Gly	Gln
			100					105					110		
Val	Ala	Ile	Ile	Ala	Asp	Val	Asp	Glu	Arg	Thr	Arg	Lys	Thr	Gly	Glu
		115					120					125			
Ala	Phe	Ala	Ala	Gly	Leu	Ala	Pro	Asp	Cys	Ala	Ile	Thr	Val	Arg	Thr
	130					135						140			
Gln	Ala	Asp	Thr	Ser	Ser	Pro	Asp	Pro	Leu	Phe	Asn	Pro	Leu	Lys	Thr
145					150					155					160
Gly	Val	Cys	Gln	Leu	Asp	Asn	Ala	Asn	Val	Thr	Asp	Ala	Ile	Leu	Ser
				165					170					175	
Arg	Ala	Gly	Gly	Ser	Ile	Ala	Asp	Phe	Thr	Gly	His	Arg	Gln	Thr	Ala
		180					185					190			
Phe	Arg	Glu	Leu	Glu	Arg	Val	Leu	Asn	Phe	Pro	Gln	Ser	Asn	Leu	Cys
	195						200					205			
Leu	Lys	Arg	Glu	Lys	Gln	Asp	Glu	Ser	Cys	Ser	Leu	Thr	Gln	Ala	Leu
	210					215					220				
Pro	Ser	Glu	Leu	Lys	Val	Ser	Ala	Asp	Asn	Val	Ser	Leu	Thr	Gly	Ala
225					230					235					240
Val	Ser	Leu	Ala	Ser	Met	Leu	Thr	Glu	Ile	Phe	Leu	Leu	Gln	Gln	Ala
				245					250					255	
Gln	Gly	Met	Pro	Glu	Pro	Gly	Trp	Gly	Arg	Ile	Thr	Asp	Ser	His	Gln
			260					265					270		
Trp	Asn	Thr	Leu	Leu	Ser	Leu	His	Asn	Ala	Gln	Phe	Tyr	Leu	Leu	Gln
		275					280					285			
Arg	Thr	Pro	Glu	Val	Ala	Arg	Ser	Arg	Ala	Thr	Pro	Leu	Leu	Asp	Leu
	290					295					300				
Ile	Lys	Thr	Ala	Leu	Thr	Pro	His	Pro	Pro	Gln	Lys	Gln	Ala	Tyr	Gly

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Val Thr Leu Pro Thr Ser Val Leu Phe Ile Ala Gly His Asp Thr Asn						
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Leu Ala Asn Leu Gly Gly Ala Leu Glu Leu Asn Trp Thr Leu Pro Gly						
	340		345		350	
Gln Pro Asp Asn Thr Pro Pro Gly Gly Glu Leu Val Phe Glu Arg Trp						
	355		360		365	
Arg Arg Leu Ser Asp Asn Ser Gln Trp Ile Gln Val Ser Leu Val Phe						
	370		375		380	
Gln Thr Leu Gln Gln Met Arg Asp Lys Thr Pro Leu Ser Leu Asn Thr						
	385		390		395	
Pro Pro Gly Glu Val Lys Leu Thr Leu Ala Gly Cys Glu Glu Arg Asn						
	405		410		415	
Ala Gln Gly Met Cys Ser Leu Ala Gly Phe Thr Gln Ile Val Asn Glu						
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Asp Ala Trp Pro Thr Trp Pro Val Lys Leu Gly Arg Leu Thr Pro Arg			
	65	70	75
Gly Gly Glu Leu Ile Ala Tyr Leu Gly His Tyr Gln Arg Gln Arg Leu			
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Val Ala Asp Gly Leu Leu Val Lys Lys Gly Cys Pro Gln Ser Gly Gln			
	100	105	110
Val Ala Ile Ile Ala Asp Val Asp Glu Arg Thr Arg Lys Thr Gly Glu			
	115	120	125
Ala Phe Ala Ala Gly Leu Ala Pro Asp Cys Ala Ile Thr Val Arg Thr			
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Gln Ala Asp Thr Ser Ser Pro Asp Pro Leu Phe Asn Pro Leu Lys Thr			
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Gly Val Cys Gln Leu Asp Asn Ala Asn Val Thr Asp Ala Ile Leu Ser			
	165	170	175
Arg Ala Gly Gly Ser Ile Ala Asp Phe Thr Gly His Arg Gln Thr Ala			
	180	185	190
Phe Arg Glu Leu Glu Arg Val Leu Asn Phe Pro Gln Ser Asn Leu Cys			
	195	200	205
Leu Lys Arg Glu Lys Gln Asp Glu Ser Cys Ser Leu Thr Gln Ala Leu			
	210	215	220
Pro Ser Glu Leu Lys Val Ser Ala Asp Asn Val Ser Leu Thr Gly Ala			
	225	230	235
			240



Val	Ser	Leu	Ala	Ser	Met	Leu	Thr	Glu	Ile	Phe	Leu	Leu	Gln	Gln	Ala
				245					250					255	
Gln	Gly	Met	Pro	Glu	Pro	Gly	Trp	Gly	Arg	Ile	Thr	Asp	Ser	His	Gln
			260					265					270		
Trp	Asn	Thr	Leu	Leu	Ser	Leu	His	Asn	Ala	Gln	Phe	Tyr	Leu	Leu	Gln
		275					280					285			
Arg	Thr	Pro	Glu	Val	Ala	Arg	Ser	Arg	Ala	Thr	Pro	Leu	Leu	Asp	Leu
	290					295					300				
Ile	Lys	Thr	Ala	Leu	Thr	Pro	His	Pro	Pro	Gln	Lys	Gln	Ala	Tyr	Gly
305					310					315					320
Val	Thr	Leu	Pro	Thr	Ser	Val	Leu	Phe	Ile	Ala	Gly	His	Asp	Thr	Asn
				325					330					335	
Leu	Ala	Asn	Leu	Gly	Gly	Ala	Leu	Glu	Leu	Asn	Trp	Thr	Leu	Pro	Gly
			340					345					350		
Gln	Pro	Asp	Asn	Thr	Pro	Pro	Gly	Gly	Glu	Leu	Val	Phe	Glu	Arg	Trp
		355					360					365			
Arg	Arg	Leu	Ser	Asp	Asn	Ser	Gln	Trp	Ile	Gln	Val	Ser	Leu	Val	Phe
	370					375					380				
Gln	Thr	Leu	Gln	Gln	Met	Arg	Asp	Lys	Thr	Pro	Leu	Ser	Leu	Asn	Thr
385					390					395					400
Pro	Pro	Gly	Glu	Val	Lys	Leu	Thr	Leu	Ala	Gly	Cys	Glu	Glu	Arg	Asn
				405					410					415	
Ala	Gln	Gly	Met	Cys	Ser	Leu	Ala	Gly	Phe	Thr	Gln	Ile	Val	Asn	Glu
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Ala	Arg	Ile	Pro	Ala	Cys	Ser	Leu								
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<223> synthetic mutant AppA PHY846 phytase

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			20					25					30		
Glu	Pro	Glu	Leu	Lys	Leu	Glu	Ser	Val	Val	Ile	Val	Ser	Arg	His	Gly
		35				40						45			
Val	Arg	Ala	Pro	Thr	Lys	Ala	Thr	Gln	Leu	Met	Gln	Asp	Val	Thr	Pro
	50					55					60				
Asp	Ala	Trp	Pro	Thr	Trp	Pro	Val	Lys	Leu	Gly	Trp	Leu	Thr	Pro	Arg
65					70					75					80
Gly	Gly	Glu	Leu	Ile	Ala	Tyr	Leu	Gly	His	Tyr	Gln	Arg	Gln	Arg	Leu
				85					90					95	
Val	Ala	Asp	Gly	Leu	Leu	Ala	Lys	Lys	Gly	Cys	Pro	Gln	Ser	Gly	Gln
		100						105					110		
Val	Ala	Ile	Ile	Ala	Asp	Val	Asp	Glu	Arg	Thr	Arg	Lys	Thr	Gly	Glu
		115					120						125		
Ala	Phe	Ala	Ala	Gly	Leu	Ala	Pro	Asp	Cys	Ala	Ile	Thr	Val	Arg	Thr
		130				135						140			
Gln	Ala	Asp	Thr	Ser	Ser	Pro	Asp	Pro	Leu	Phe	Asn	Pro	Leu	Lys	Thr
145					150					155					160
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